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☐ 1: Y11416. H.sapiens mRNA fo...[gi:2370175]

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LOCUS HSY11416 2234 bp mRNA linear PRI 02-SEP-1997

DEFINITION H.sapiens mRNA for P73.

ACCESSION Y11416

VERSION Y11416.1 GI:2370175

KEYWORDS p53 transcription factor; P73 gene; transcription factor; tumor suppressor.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kaghad,M., Bonnet,H., Yang,A., Creancier,L., Biscan,J.C., Valent,A., Minty,A., Chalon,P., Lelias,J.M., Dumont,X., Ferrara,P., McKeon,F. and Caput,D.

TITLE Monoallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers

JOURNAL Cell 90 (4), 809-819 (1997)

MEDLINE [97433090](#)

PUBMED [9288759](#)

REFERENCE 2 (bases 1 to 2234)

AUTHORS Caput,D.

TITLE Direct Submission

JOURNAL Submitted (21-FEB-1997) D. Caput, Sanofi-Elf-Bio-Recherches, Labège Innopole - BP 137- Voie N 1, 31676, Labège Cedex, FRANCE

FEATURES

Location/Qualifiers

source 1..2234

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/chromosome="1"

/map="p36"

/cell\_line="HT29"

/cell\_type="adenocarcinoma colon"

mRNA <1..>2234

/evidence=experimental

variation 78..175

/note="exon 2 deletion second splice variant"

variation 81

/note="allelic variant"

/replace="a"

variation 91

/note="allelic variant"

/replace="t"

gene 111..2021

CDS

```

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111..2021
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/db_xref="SPTREMBL:015350"
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QIKVSTPPPPGTAIRAMPVYKKAHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVE
GNNLSQYVDDPVTGRQSVVVPYEPQVGTEFTTILYNFMCNSSCVGGMNRRLILIT
LEMRDGGVLGRRSFEGRIACPCGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSP
PAVPALGAGVKKRRHGDDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQ
QQLLQRPSHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGP
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FTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDYSTAQQLLRSSNA
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CDS

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QIKVSTPPPPGTAIRAMPVYKKAHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVE
GNNLSQYVDDPVTGRQSVVVPYEPQVGTEFTTILYNFMCNSSCVGGMNRRLILIT
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QQLLQRPSHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGP
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CDS

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/db_xref="SPTREMBL:015350"
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NRRLILITLEMRDGGVLGRRSFEGRIACPCGRDRKADEDHYREQQALNESSAKNGA
ASKRAFKQSPPAVPALGAGVKKRRHGDDEDTYYLQVRGRENFEILMKLKESLELMELVP
QPLVDSYRQQQLLQRPSHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSA
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variation

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1595..1688
/gene="P73"

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/note="exon 13 deletion  
first splice variant"

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121	ccaccgccac	ctcccctgat	gggggcacca	cgtttgagca
181	cagacagcac	ctacttcgac	cttccccagt	caagccgggg
241	gaacggattc	cagcatggac	gtcttccacc	tggagggcac
301	agttcaatct	gctgagcagc	accatggacc	agatgagcag
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481	cccaccactt	tgaggtcact	ttccagcagt	ccagcacggc
541	actccccgct	cttgaagaaa	cttactgcc	agatcgccaa
601	aggtgtccac	cccgccaccc	ccaggcactg	ccatccgggc
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721	acgaaggaca	gtctgtctca	gccagccacc	tcacccgct
781	agtatgtgga	tgaccctgtc	accggcaggc	agagcgtcgt
841	aggtggggac	ggaattcacc	accatcctgt	acaacttcat
901	ggggcatgaa	ccggcgcccc	atcctcatca	tcacccct
961	tgctggggcg	ccggttcctt	gagggccgca	tcctggcccg
1021	ctgatgagga	ccactaccgg	gagcagcagg	ccctgaacga
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1201	actttgagat	cctgatgaag	ctgaaagaga	gcctggagct
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1381	tgccctccgt	caaccagctg	gtgggcccagc	ctccccgca
1441	acctggggcc	cgtgggcccc	gggatgtca	acaacctatg
1501	gcgagatgag	cagcagccac	agcgcccagt	ccatggtctc
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1681	ccattgagga	cctggggggc	ctgaagatcc	ccgagcagta
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1801	gcaacgcggc	caccatctcc	atcgggcggt	caggggaaact
1861	aggccgtgca	cttccgcgtg	cgccacacca	tcaccatccc
1921	gcggccctga	cgagtgggcg	gacttcggct	tcgacctgcc
1981	agcccatcaa	ggaggagttc	acggaggccg	agatccactg
2041	cctgcgccac	cgcccagaga	cccaagctgc	ctccccctc
2101	gcctcaggag	gcaggacctt	cgggctgtgc	ccggggaaag
2161	aggcacctca	caggccccag	gaaaggccca	gccaccgaag
2221	tcacctgcag	aacc		

//

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Jun 19 2003 12:37:45

Score = 123 bits (62), Expect = 1e-25  
Identities = 170/206 (82%)  
Strand = Plus / Plus

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 ||||| || ||||| ||||| |||||  
 Sbjct: 681 gtgaaacgctgccccaccacgagct 706

7/3/03

Score = 123 bits (62), Expect = 1e-25  
Identities = 170/206 (82%)  
Strand = Plus / Plus

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Sbjct: 681  gtgaaacgctgccccaaccacgagct 706
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Score = 123 bits (62), Expect = 1e-25  
Identities = 170/206 (82%)  
Strand = Plus / Plus

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Query: 218 gtgaagcgggtccccaaccatgagct 243
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Sbjct: 681 gtgaaacgctgccccaaccacgagct 706
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caccgactac

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541 ccaggcccg acagtttcga cgtgtccttc cagcagtcga gcaccgcca gtcggccacc
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661 cagatcaagg tgatgacccc acctcctcag ggagctgtta tccgcgcat gcctgtctac
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AB016072